

## SEQUENCE LISTING

10/516662  
#9  
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<110> University of Utah Research Foundation  
Bock, Susan C.  
Hobden, Adrian N.

<120> VARIANTS OF ANTITHROMBIN III

<130> 21101.0021P1

<150> 60/384,599

<151> 2002-05-31

<160> 93

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## synthetic construct

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<210> 65

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Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu Asp Glu  
20 25 30  
Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val Trp Glu  
35 40 45  
Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln His Leu  
50 55 60  
Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro Leu Ser  
65 70 75 80  
Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr  
85 90 95  
Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys  
100 105 110  
Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys Arg Leu  
115 120 125  
Tyr Arg Lys Ala Asn Lys Ala Ser Lys Leu Val Ser Ala Asn Arg Leu  
130 135 140  
Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp Ile Ser  
145 150 155 160  
Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys Glu Asn  
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29

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26

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Page 15

## synthetic construct

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Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu Asp Glu  
20 25 30  
Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val Trp Glu  
35 40 45  
Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln His Leu  
50 55 60  
Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro Leu Ser  
65 70 75 80  
Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr  
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Leu	Gln	Gln	Leu	85	Met	Glu	Val	Phe	Lys	90	Phe	Asp	Thr	Ile	Ser	95	Glu	Lys
Thr	Ser	Asp	100	Gln	Ile	His	Phe	Phe	105	Phe	Ala	Lys	Leu	Asn	110	Cys	Arg	Leu
Tyr	Arg	115	Lys	Ala	Asn	Lys	Ala	120	Ser	Lys	Leu	Val	Ser	125	Ala	Asn	Arg	Leu
Phe	Gly	130	Asp	Lys	Ser	Leu	Thr	135	Phe	Asn	Glu	Thr	Tyr	140	Gln	Asp	Ile	Ser
145	Glu	Leu	Val	Tyr	Gly	150	Ala	Lys	Leu	Gln	Pro	Leu	Asp	155	Phe	Lys	Glu	Asn
Ala	Glu	Gln	Ser	160	Arg	Ala	Ala	Ile	Asn	165	Lys	Trp	Val	Ser	170	Asn	Lys	Thr
Glu	Gly	Arg	180	Ile	Thr	Asp	Val	Ile	Pro	185	Ser	Glu	Ala	Ile	200	Asn	Glu	Leu
Thr	Val	195	Leu	Val	Leu	Val	Asn	Thr	Ile	210	Tyr	Phe	Lys	Gly	220	Leu	Trp	Lys
Ser	Lys	Phe	Ser	Pro	Glu	Asn	Thr	Arg	Lys	215	Glu	Leu	Phe	Tyr	225	Lys	Ala	240
Asp	Gly	Glu	Ser	Cys	230	Ser	Ala	Ser	Met	235	Tyr	Gln	Glu	Gly	245	Lys	Phe	255
Arg	Tyr	Arg	Arg	Val	Ala	Glu	Gly	Thr	Gln	250	Val	Leu	Glu	Leu	255	Pro	Phe	270
Lys	Gly	Asp	260	Ile	Thr	Met	Val	Leu	Ile	265	Leu	Pro	Lys	Pro	275	Glu	Lys	285
Ser	Leu	Ala	Lys	Val	Glu	Lys	Glu	Leu	Thr	280	Pro	Glu	Val	Leu	285	Gln	Glu	300
Trp	Leu	Asp	Glu	Leu	Glu	310	Glu	Met	Met	315	Val	Val	His	Met	320	Pro	Arg	330
Phe	Arg	Ile	Glu	Asp	Gly	Phe	Ser	Leu	Lys	325	Glu	Gln	Leu	Gln	330	Asp	Met	335
Gly	Leu	Val	Asp	Leu	Phe	Ser	Pro	Glu	Lys	340	Ser	Lys	Leu	Pro	345	Gly	Ile	350
Val	Ala	Glu	Gly	Arg	Asp	Asp	Leu	Tyr	Val	355	Ser	Asp	Ala	Phe	360	His	Lys	365
Ala	Phe	Leu	Glu	Val	Asn	Glu	Glu	Gly	Ser	370	Glu	Ala	Ala	Ala	375	Ser	Thr	380
Ala	Leu	Glu	Ala	Gln	Gly	Arg	Ser	Leu	Asn	385	Pro	Asn	Arg	Val	390	Thr	Phe	400
Lys	Ala	Asn	Arg	Pro	Phe	Leu	Val	Phe	Ile	405	Arg	Glu	Val	Pro	410	Leu	Asn	415
Thr	Ile	Ile	Phe	Met	Gly	Arg	Val	Ala	Asn	420	Pro	Cys	Val	Lys	425	Lys		430

&lt;210&gt; 78

&lt;211&gt; 430

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 78

Ser	Pro	Val	Asp	Ile	Cys	Thr	Ala	Lys	Pro	Arg	Asp	Ile	Pro	Met	Asn
1				5					10				15		
Pro	Met	Cys	Ile	Tyr	Arg	Ser	Pro	Glu	Lys	Lys	Ala	Thr	Glu	Asp	Glu
			20					25					30		
Gly	Ser	Glu	Gln	Lys	Ile	Pro	Glu	Ala	Thr	Asn	Arg	Arg	Val	Trp	Glu
			35				40					45			
Leu	Ser	Lys	Ala	Asn	Ser	Arg	Phe	Ala	Thr	Thr	Phe	Tyr	Gln	His	Leu
			50			55					60				
Ala	Asp	Ser	Lys	Asn	Asp	Asn	Asp	Asn	Ile	Phe	Leu	Ser	Pro	Leu	Ser

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65      70      75      80
Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr
      85      90      95
Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys
      100      105      110
Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys Arg Leu
      115      120      125
Tyr Arg Lys Ala Asn Lys Ala Ser Lys Leu Val Ser Ala Asn Arg Leu
      130      135      140
Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp Ile Ser
      145      150      155
Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys Glu Asn
      160      165      170
Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr
      175      180      185
Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu
      190      195      200
Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys
      205      210      215
Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala
      220      225      230
Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly Lys Phe
      235      240      245
Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu Pro Phe
      250      255      260
Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro Glu Lys
      265      270      275
Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu
      280      285      290
Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met Pro Arg
      295      300      305
Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met
      310      315      320
Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile
      325      330      335
Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe His Lys
      340      345      350
Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr
      355      360      365
Ala Leu Glu Ala His Gly Arg Ser Leu Asn Pro Asn Arg Val Thr Phe
      370      375      380
      385      390      395
Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn
      400      405      410
Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
      415      420      425      430

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<210> 79

<211> 1293

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 79

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agccctgtgg acatctgcac agccaagccg cgggacattc ccatgaatcc catgtgcatt      60
taccgctccc cggagaagaa ggcaactgag gatgagggct cagaacagaa gatcccgag      120
gccaccaacc ggcgtgtctg ggaactgtcc aaggccaatt cccgctttgc taccactttc      180
tatcagcacc tggcagattc caagaatgac aatgataaca ttttcctgtc acccctgagt      240
atctccacgg ctittgctat gaccaagctg ggtgcctgta atgacaccct ccagcaactg      300
atggaggtat ttaagtttga caccatatct gagaaaaacat ctgatcagat ccacttcttc      360
tttgccaaac tgaactgccg actctatcga aaagccaaca aagcctccaa gttagtatca      420

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gccaatcgcc	tttttggaga	caaatccctt	accttcaatg	agacctacca	ggacatcagt	480
gagttgggtat	atggagccaa	gctccagccc	ctggacttca	aggaaaatgc	agagcaatcc	540
agagcgcca	tcaacaaatg	ggtgtccaat	aagaccgaag	gccgaatcac	cgatgtcatt	600
ccctcggaag	ccatcaatga	gctcactgtt	ctggtgctgg	ttaacacccat	ttacttcaag	660
ggcctgtgga	agtcaaagtt	cagccctgag	aacacaagga	aggaactgtt	ctacaaggct	720
gatggagagt	cgtgttcagc	atctatgatg	taccaggaag	gcaagttccg	ttatcggcgc	780
gtggctgaag	gcacccaggt	gcttgagttg	cccttcaaag	gtgatgacat	caccatgggtc	840
ctcatcttgc	ccaagcctga	gaagagcctg	gccaagggtg	agaaggaact	caccccagag	900
gtgctgcagg	agtggctgga	tgaattggag	gagatgatgc	tggtggtcca	catgccccgc	960
ttccgcattg	aggacggctt	cagtttgaag	gagcagctgc	aagacatggg	ccttgtcgat	1020
ctgttcagcc	ctgaaaagtc	caaactccca	ggattgttgg	cagaaggccg	agatgacctc	1080
tatgtctcag	atgcattcca	taaggcattt	cttgaggtaa	atgaagaagg	cagtgaagcg	1140
gccgcaagta	ccgctctaga	ggctcagggc	cgttcgctaa	acccaacag	ggtgactttc	1200
aaggccaaca	ggcctttcct	ggtttttata	agagaagttc	ctctgaacac	tattatcttc	1260
atgggcagag	tagccaaccc	ttgtgttaag	taa			1293

&lt;210&gt; 80

&lt;211&gt; 1293

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 80

agtccccgtag	atatatgcac	agccaagccg	cgggacattc	ccatgaatcc	catgtgcatt	60
taccgctccc	cggagaagaa	ggcaactgag	gatgagggct	cagaacagaa	gatccccggag	120
gccaccaaac	ggcgtgtctg	ggaactgtcc	aaggccaatt	cccgccttgc	taccactttc	180
tatcagcacc	tggcagattc	caagaatgac	aatgataaca	ttttcctgtc	acccttgagt	240
atctccacgg	cttttgctat	gaccaagctg	ggtgcctgta	atgacaccct	ccagcaactg	300
atggaggtat	ttaagtttga	caccatatct	gagaaaaacat	ctgatcagat	ccacttcttc	360
tttgccaaac	tgaactgccc	actctatcga	aaagccaaca	aagcctccaa	gttagtatca	420
gccaatcgcc	tttttggaga	caaatccctt	accttcaatg	agacctacca	ggacatcagt	480
gagttgggtat	atggagccaa	gctccagccc	ctggacttca	aggaaaatgc	agagcaatcc	540
agagcgcca	tcaacaaatg	ggtgtccaat	aagaccgaag	gccgaatcac	cgatgtcatt	600
ccctcggaag	ccatcaatga	gctcactgtt	ctggtgctgg	ttaacacccat	ttacttcaag	660
ggcctgtgga	agtcaaagtt	cagccctgag	aacacaagga	aggaactgtt	ctacaaggct	720
gatggagagt	cgtgttcagc	atctatgatg	taccaggaag	gcaagttccg	ttatcggcgc	780
gtggctgaag	gcacccaggt	gcttgagttg	cccttcaaag	gtgatgacat	caccatgggtc	840
ctcatcttgc	ccaagcctga	gaagagcctg	gccaagggtg	agaaggaact	caccccagag	900
gtgctgcagg	agtggctgga	tgaattggag	gagatgatgc	tggtggtcca	catgccccgc	960
ttccgcattg	aggacggctt	cagtttgaag	gagcagctgc	aagacatggg	ccttgtcgat	1020
ctgttcagcc	ctgaaaagtc	caaactccca	ggattgttgg	cagaaggccg	agatgacctc	1080
tatgtctcag	atgcattcca	taaggcattt	cttgaggtaa	atgaagaagg	cagtgaagcg	1140
gccgcaagta	ccgctctaga	ggctcagggc	cgttcgctaa	acccaacag	ggtgactttc	1200
aaggccaaca	ggcctttcct	ggtttttata	agagaagttc	ctctgaacac	tattatcttc	1260
atgggcagag	tagccaaccc	ttgtgttaag	taa			1293

&lt;210&gt; 81

&lt;211&gt; 430

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 81

Ser	Pro	Val	Asp	Val	Cys	Thr	Ala	Lys	Pro	Arg	Asp	Ile	Pro	Met	Asn
1				5					10					15	
Pro	Met	Cys	Ile	Tyr	Arg	Ser	Pro	Glu	Lys	Lys	Ala	Thr	Glu	Asp	Glu
			20					25					30		

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Gly	Ser	Glu	Gln	Lys	Ile	Pro	Glu	Ala	Thr	Asn	Arg	Val	Trp	Glu
		35					40				45			
Leu	Ser	Lys	Ala	Asn	Ser	Arg	Phe	Ala	Thr	Thr	Phe	Tyr	Gln	His
	50					55					60			
Ala	Asp	Ser	Lys	Asn	Asp	Asn	Asp	Asn	Ile	Phe	Leu	Ser	Pro	Leu
	65				70					75				80
Ile	Ser	Thr	Ala	Phe	Ala	Met	Thr	Lys	Leu	Gly	Ala	Cys	Asn	Asp
				85					90					95
Leu	Gln	Gln	Leu	Met	Glu	Val	Phe	Lys	Phe	Asp	Thr	Ile	Ser	Glu
			100					105					110	
Thr	Ser	Asp	Gln	Ile	His	Phe	Phe	Ala	Lys	Leu	Asn	Cys	Arg	Leu
		115				120					125			
Tyr	Arg	Lys	Ala	Asn	Lys	Ala	Ser	Lys	Leu	Val	Ser	Ala	Asn	Arg
	130					135					140			
Phe	Gly	Asp	Lys	Ser	Leu	Thr	Phe	Asn	Glu	Thr	Tyr	Gln	Asp	Ile
	145				150					155				160
Glu	Leu	Val	Tyr	Gly	Ala	Lys	Leu	Gln	Pro	Leu	Asp	Phe	Lys	Glu
				165					170					175
Ala	Glu	Gln	Ser	Arg	Ala	Ala	Ile	Asn	Lys	Trp	Val	Ser	Asn	Lys
			180					185					190	
Glu	Gly	Arg	Ile	Thr	Asp	Val	Ile	Pro	Ser	Glu	Ala	Ile	Asn	Glu
		195					200					205		
Thr	Val	Leu	Val	Leu	Val	Asn	Thr	Ile	Tyr	Phe	Lys	Gly	Leu	Trp
	210					215					220			
Ser	Lys	Phe	Ser	Pro	Glu	Asn	Thr	Arg	Lys	Glu	Leu	Phe	Tyr	Lys
	225				230					235				240
Asp	Gly	Glu	Ser	Cys	Ser	Ala	Ser	Met	Met	Tyr	Gln	Glu	Gly	Lys
				245					250					255
Arg	Tyr	Arg	Arg	Val	Ala	Glu	Gly	Thr	Gln	Val	Leu	Glu	Leu	Pro
			260					265					270	
Lys	Gly	Asp	Asp	Ile	Thr	Met	Val	Leu	Ile	Leu	Pro	Lys	Pro	Glu
		275				280						285		
Ser	Leu	Ala	Lys	Val	Glu	Lys	Glu	Leu	Thr	Pro	Glu	Val	Leu	Gln
	290					295					300			
Trp	Leu	Asp	Glu	Leu	Glu	Glu	Met	Met	Leu	Val	Val	His	Met	Pro
	305				310					315				320
Phe	Arg	Ile	Glu	Asp	Gly	Phe	Ser	Leu	Lys	Glu	Gln	Leu	Gln	Asp
				325					330					335
Gly	Leu	Val	Asp	Leu	Phe	Ser	Pro	Glu	Lys	Ser	Lys	Leu	Pro	Gly
			340					345					350	
Val	Ala	Glu	Gly	Arg	Asp	Asp	Leu	Tyr	Val	Ser	Asp	Ala	Phe	His
		355					360					365		
Ala	Phe	Leu	Glu	Val	Asn	Glu	Glu	Gly	Ser	Glu	Ala	Ala	Ala	Ser
	370					375					380			
Ala	Leu	Glu	Ala	Gln	Gly	Arg	Ser	Leu	Asn	Pro	Asn	Arg	Val	Thr
	385				390					395				400
Lys	Ala	Asn	Arg	Pro	Phe	Leu	Val	Phe	Ile	Arg	Glu	Val	Pro	Leu
				405					410					415
Thr	Ile	Ile	Phe	Met	Gly	Arg	Val	Ala	Asn	Pro	Cys	Val	Lys	
			420					425					430	

<210> 82

<211> 1293

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 82

agccctgtgg acgtatgcac agccaagccg cgggacattc ccatgaatcc catgtgcatt

60

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taccgctccc	cggagaagaa	ggcaactgag	gatgagggct	cagaacagaa	gatccccggag	120
gccaccaacc	ggcgtgtctg	ggaactgtcc	aaggccaatt	cccgccttgc	taccacttttc	180
tatcagcacc	tggcagattc	caagaatgac	aatgataaca	ttttcctgtc	acccttgagt	240
atctccacgg	cttttgctat	gaccaagctg	ggtgcctgta	atgacaccct	ccagcaactg	300
atggaggtat	ttaagtttga	caccatatct	gagaaaacat	ctgatcagat	ccacttcttc	360
tttgccaaac	tgaactgccg	actctatcga	aaagccaaca	aagcctccaa	gttagtatca	420
gccaatcgcc	tttttgga	caaatccctt	accttcaatg	agacctacca	ggacatcagt	480
gagttggtat	atggagccaa	gctccagccc	ctggacttca	aggaaaatgc	agagcaatcc	540
agagcggcc	tcaacaaatg	ggtgtccaat	aagaccgaag	gccgaatcac	cgatgtcatt	600
ccctcggaag	ccatcaatga	gctcactggt	ctggtgctgg	ttaacaccat	ttacttcaag	660
ggcctgtgga	agtcaaagtt	cagccctgag	aacacaagga	aggaactggt	ctacaaggct	720
gatggagagt	cgtgttcagc	atctatgatg	taccaggaag	gcaagttccg	ttatcggcgc	780
gtggctgaag	gcacccaggt	gcttgagttg	cccttcaaag	gtgatgacat	caccatgggtc	840
ctcatcttgc	ccaagcctga	gaagagcctg	gccaaggtgg	agaaggaact	cacccagag	900
gtgctgcagg	agtggctgga	tgaattggag	gagatgatgc	tggtggtcca	catgccccgc	960
ttccgcattg	aggacggctt	cagtttgaag	gagcagctgc	aagacatggg	ccttgctgat	1020
ctgttcagcc	ctgaaaagtc	caaactccca	ggtattgttg	cagaaggccg	agatgacctc	1080
tatgtctcag	atgcattcca	taaggcattt	cttgaggtaa	atgaagaagg	cagtgaagcg	1140
gccgcaagta	ccgctctaga	ggctcagggc	cgttcgctaa	acccaacag	ggtgactttc	1200
aaggccaaca	ggcctttcct	ggtttttata	agagaagttc	ctctgaacac	tattatcttc	1260
atgggcagag	tagccaaccc	ttgtgttaag	taa			1293

&lt;210&gt; 83

&lt;211&gt; 1293

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 83

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taccgctccc	cggagaagaa	ggcaactgag	gatgagggct	cagaacagaa	gatccccggag	120
gccaccaacc	ggcgtgtctg	ggaactgtcc	aaggccaatt	cccgccttgc	taccacttttc	180
tatcagcacc	tggcagattc	caagaatgac	aatgataaca	ttttcctgtc	acccttgagt	240
atctccacgg	cttttgctat	gaccaagctg	ggtgcctgta	atgacaccct	ccagcaactg	300
atggaggtat	ttaagtttga	caccatatct	gagaaaacat	ctgatcagat	ccacttcttc	360
tttgccaaac	tgaactgccg	actctatcga	aaagccaaca	aagcctccaa	gttagtatca	420
gccaatcgcc	tttttgga	caaatccctt	accttcaatg	agacctacca	ggacatcagt	480
gagttggtat	atggagccaa	gctccagccc	ctggacttca	aggaaaatgc	agagcaatcc	540
agagcggcc	tcaacaaatg	ggtgtccaat	aagaccgaag	gccgaatcac	cgatgtcatt	600
ccctcggaag	ccatcaatga	gctcactggt	ctggtgctgg	ttaacaccat	ttacttcaag	660
ggcctgtgga	agtcaaagtt	cagccctgag	aacacaagga	aggaactggt	ctacaaggct	720
gatggagagt	cgtgttcagc	atctatgatg	taccaggaag	gcaagttccg	ttatcggcgc	780
gtggctgaag	gcacccaggt	gcttgagttg	cccttcaaag	gtgatgacat	caccatgggtc	840
ctcatcttgc	ccaagcctga	gaagagcctg	gccaaggtgg	agaaggaact	cacccagag	900
gtgctgcagg	agtggctgga	tgaattggag	gagatgatgc	tggtggtcca	catgccccgc	960
ttccgcattg	aggacggctt	cagtttgaag	gagcagctgc	aagacatggg	ccttgctgat	1020
ctgttcagcc	ctgaaaagtc	caaactccca	ggtattgttg	cagaaggccg	agatgacctc	1080
tatgtctcag	atgcattcca	taaggcattt	cttgaggtaa	atgaagaagg	cagtgaagcg	1140
gccgcaagta	ccgctctaga	ggctcagggc	cgttcgctaa	acccaacag	ggtgactttc	1200
aaggccaaca	ggcctttcct	ggtttttata	agagaagttc	ctctgaacac	tattatcttc	1260
atgggcagag	tagccaaccc	ttgtgttaag	taa			1293

&lt;210&gt; 84

&lt;211&gt; 430

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

## 246416\_1.txt

&lt;400&gt; 84

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Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro Met Asn
1      5      10      15
Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu Asp Glu
20      25      30
Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val Trp Glu
35      40      45
Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln His Leu
50      55      60
Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro Leu Ser
65      70      75      80
Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr
85      90      95
Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys
100      105      110
Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys Arg Leu
115      120      125

Tyr Arg Lys Ala Asn Lys Ala Ser Lys Leu Val Ser Ala Asn Arg Leu
130      135      140
Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp Ile Ser
145      150      155      160
Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys Glu Asn
165      170      175
Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr
180      185      190
Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu
195      200      205
Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys
210      215      220
Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala
225      230      235      240
Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly Lys Phe
245      250      255
Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu Pro Phe
260      265      270
Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro Glu Lys
275      280      285
Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu
290      295      300
Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met Pro Arg
305      310      315      320
Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met
325      330      335
Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile
340      345      350
Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe His Lys
355      360      365
Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr
370      375      380
Ala Leu Glu Ala Tyr Gly Arg Ser Leu Asn Pro Asn Arg Val Thr Phe
385      390      395      400
Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn
405      410      415
Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
420      425      430

```

&lt;210&gt; 85

&lt;211&gt; 432

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 85

His 1	Gly	Ser	Pro	Val 5	Asp	Ile	Cys	Thr	Ala 10	Lys	Pro	Arg	Asp	Ile 15	Pro
Met	Asn	Pro	Met 20	Cys	Ile	Tyr	Arg	Ser 25	Pro	Glu	Lys	Lys	Ala 30	Thr	Glu
Asp	Glu	Gly 35	Ser	Glu	Gln	Lys	Ile 40	Pro	Glu	Ala	Thr	Asn 45	Arg	Arg	Val
Trp 50	Glu	Leu	Ser	Lys	Ala 55	Asn	Ser	Arg	Phe	Ala	Thr 60	Thr	Phe	Tyr	Gln
His 65	Leu	Ala	Asp	Ser 70	Lys	Asn	Asp	Asn	Asp 75	Asn	Ile	Phe	Leu	Ser 80	Pro
Leu	Ser	Ile	Ser	Thr 85	Ala	Phe	Ala	Met	Thr 90	Lys	Leu	Gly	Ala 95	Cys	Asn
Asp	Thr	Leu	Gln 100	Gln	Leu	Met	Glu	Val 105	Phe	Lys	Phe	Asp	Thr 110	Ile	Ser
Glu	Lys	Thr 115	Ser	Asp	Gln	Ile	His 120	Phe	Phe	Ala	Lys 125	Leu	Asn	Cys	
Arg 130	Leu	Tyr	Arg	Lys	Ala 135	Asn	Lys	Ser	Ser	Lys	Leu 140	Val	Ser	Ala	Asn
Arg 145	Leu	Phe	Gly	Asp 150	Lys	Ser	Leu	Thr	Phe	Asn 155	Glu	Thr	Tyr	Gln	Asp 160
Ile	Ser	Glu	Leu 165	Val	Tyr	Gly	Ala	Lys	Leu 170	Gln	Pro	Leu	Asp	Phe 175	Lys
Glu	Asn	Ala	Glu 180	Gln	Ser	Arg	Ala	Ala 185	Ile	Asn	Lys	Trp	Val 190	Ser	Asn
Lys	Thr	Glu 195	Gly	Arg	Ile	Thr	Asp 200	Val	Ile	Pro	Ser	Glu 205	Ala	Ile	Asn
Glu 210	Leu	Thr	Val	Leu	Val	Leu 215	Val	Asn	Thr	Ile	Tyr 220	Phe	Lys	Gly	Leu
Trp 225	Lys	Ser	Lys	Phe 230	Ser	Pro	Glu	Asn	Thr	Arg 235	Lys	Glu	Leu	Phe	Tyr 240
Lys	Ala	Asp	Gly	Glu 245	Ser	Cys	Ser	Ala	Ser 250	Met	Met	Tyr	Gln	Glu 255	Gly
Lys	Phe	Arg	Tyr 260	Arg	Arg	Val	Ala	Glu 265	Gly	Thr	Gln	Val	Leu 270	Glu	Leu
Pro	Phe	Lys 275	Gly	Asp	Asp	Ile	Thr 280	Met	Val	Leu	Ile	Leu 285	Pro	Lys	Pro
Glu	Lys	Ser	Leu	Ala	Lys	Val 295	Glu	Lys	Glu	Leu	Thr 300	Pro	Glu	Val	Leu
Gln 305	Glu	Trp	Leu	Asp 310	Glu	Leu	Glu	Glu	Met	Met 315	Leu	Val	Val	His	Met 320
Pro	Arg	Phe	Arg	Ile 325	Glu	Asp	Gly	Phe	Ser 330	Leu	Lys	Glu	Gln	Leu 335	Gln
Asp	Met	Gly	Leu 340	Val	Asp	Leu	Phe	Ser 345	Pro	Glu	Lys	Ser	Lys 350	Leu	Pro
Gly	Ile	Val 355	Ala	Glu	Gly	Arg	Asp 360	Asp	Leu	Tyr	Val	Ser 365	Asp	Ala	Phe
His 370	Lys	Ala	Phe	Leu	Glu	Val 375	Asn	Glu	Glu	Gly	Ser 380	Glu	Ala	Ala	Ala
Ser 385	Thr	Ala	Leu	Glu	Ala 390	Gln	Gly	Arg	Ser	Leu 395	Asn	Pro	Asn	Arg	Val 400
Thr	Phe	Lys	Ala	Asn 405	Arg	Pro	Phe	Leu	Val 410	Phe	Ile	Arg	Glu	Val 415	Pro
Leu	Asn	Thr	Ile 420	Ile	Phe	Met	Gly	Arg 425	Val	Ala	Asn	Pro	Cys 430	Val	Lys

&lt;210&gt; 86

&lt;211&gt; 432

&lt;212&gt; PRT

## &lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 86

His	Gly	Ser	Pro	Val	Asp	Ile	Cys	Thr	Ala	Lys	Pro	Arg	Asp	Ile	Pro
1				5					10					15	
Met	Asn	Pro	Met	Cys	Ile	Tyr	Arg	Ser	Pro	Glu	Lys	Lys	Ala	Thr	Glu
			20					25					30		
Asp	Glu	Gly	Ser	Glu	Gln	Lys	Ile	Pro	Glu	Ala	Thr	Asn	Arg	Arg	Val
		35					40					45			
Trp	Glu	Leu	Ser	Lys	Ala	Asn	Ser	Arg	Phe	Ala	Thr	Thr	Phe	Tyr	Gln
	50					55					60				
His	Leu	Ala	Asp	Ser	Lys	Asn	Asp	Asn	Asp	Asn	Ile	Phe	Leu	Ser	Pro
65					70				75					80	
Leu	Ser	Ile	Ser	Thr	Ala	Phe	Ala	Met	Thr	Lys	Leu	Gly	Ala	Cys	Asn
				85					90					95	
Asp	Thr	Leu	Gln	Gln	Leu	Met	Glu	Val	Phe	Lys	Phe	Asp	Thr	Ile	Ser
			100					105					110		
Glu	Lys	Thr	Ser	Asp	Gln	Ile	His	Phe	Phe	Phe	Ala	Lys	Leu	Asn	Cys
		115					120					125			
Arg	Leu	Tyr	Arg	Lys	Ala	Asn	Lys	Ser	Ser	Lys	Leu	Val	Ser	Ala	Asn
						135					140				
Arg	Leu	Phe	Gly	Asp	Lys	Ser	Leu	Thr	Phe	Asn	Glu	Thr	Tyr	Gln	Asp
145					150					155					160
Ile	Ser	Glu	Leu	Val	Tyr	Gly	Ala	Lys	Leu	Gln	Pro	Leu	Asp	Phe	Lys
				165					170					175	
Glu	Asn	Ala	Glu	Gln	Ser	Arg	Ala	Ala	Ile	Asn	Lys	Trp	Val	Ser	Asn
			180					185					190		
Lys	Thr	Glu	Gly	Arg	Ile	Thr	Asp	Val	Ile	Pro	Ser	Glu	Ala	Ile	Asn
		195					200					205			
Glu	Leu	Thr	Val	Leu	Val	Leu	Val	Asn	Thr	Ile	Tyr	Phe	Lys	Gly	Leu
	210					215					220				
Trp	Lys	Ser	Lys	Phe	Ser	Pro	Glu	Asn	Thr	Arg	Lys	Glu	Leu	Phe	Tyr
225					230					235					240
Lys	Ala	Asp	Gly	Glu	Ser	Cys	Ser	Ala	Ser	Met	Met	Tyr	Gln	Glu	Gly
				245					250					255	
Lys	Phe	Arg	Tyr	Arg	Arg	Val	Ala	Glu	Gly	Thr	Gln	Val	Leu	Glu	Leu
			260					265					270		
Pro	Phe	Lys	Gly	Asp	Asp	Ile	Thr	Met	Val	Leu	Ile	Leu	Pro	Lys	Pro
		275					280					285			
Glu	Lys	Ser	Leu	Ala	Lys	Val	Glu	Lys	Glu	Leu	Thr	Pro	Glu	Val	Leu
	290					295					300				
Gln	Glu	Trp	Leu	Asp	Glu	Leu	Glu	Glu	Met	Met	Leu	Val	Val	His	Met
305					310					315					320
Pro	Arg	Phe	Arg	Ile	Glu	Asp	Gly	Phe	Ser	Leu	Lys	Glu	Gln	Leu	Gln
				325					330					335	
Asp	Met	Gly	Leu	Val	Asp	Leu	Phe	Ser	Pro	Glu	Lys	Ser	Lys	Leu	Pro
			340					345					350		
Gly	Ile	Val	Ala	Glu	Gly	Arg	Asp	Asp	Leu	Tyr	Val	Ser	Asp	Ala	Phe
		355					360					365			
His	Lys	Ala	Phe	Leu	Glu	Val	Asn	Glu	Glu	Gly	Ser	Glu	Ala	Ala	Ala
	370					375					380				
Ser	Thr	Ala	Leu	Glu	Ala	His	Gly	Arg	Ser	Leu	Asn	Pro	Asn	Arg	Val
					390					395					400
Thr	Phe	Lys	Ala	Asn	Arg	Pro	Phe	Leu	Val	Phe	Ile	Arg	Glu	Val	Pro
				405					410					415	
Leu	Asn	Thr	Ile	Ile	Phe	Met	Gly	Arg	Val	Ala	Asn	Pro	Cys	Val	Lys
			420					425					430		



## 246416\_1.txt

<210> 87  
 <211> 432  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/note =  
 synthetic construct

<400> 87

His	Gly	Ser	Pro	Val	Asp	Ile	Cys	Thr	Ala	Lys	Pro	Arg	Asp	Ile	Pro
1				5					10					15	
Met	Asn	Pro	Met	Cys	Ile	Tyr	Arg	Ser	Pro	Glu	Lys	Lys	Ala	Thr	Glu
			20					25					30		
Asp	Glu	Gly	Ser	Glu	Gln	Lys	Ile	Pro	Glu	Ala	Thr	Asn	Arg	Arg	Val
		35				40						45			
Trp	Glu	Leu	Ser	Lys	Ala	Asn	Ser	Arg	Phe	Ala	Thr	Thr	Phe	Tyr	Gln
	50					55					60				
His	Leu	Ala	Asp	Ser	Lys	Asn	Asp	Asn	Asp	Asn	Ile	Phe	Leu	Ser	Pro
65					70				75					80	
Leu	Ser	Ile	Ser	Thr	Ala	Phe	Ala	Met	Thr	Lys	Leu	Gly	Ala	Cys	Asn
				85					90				95		
Asp	Thr	Leu	Gln	Gln	Leu	Met	Glu	Val	Phe	Lys	Phe	Asp	Thr	Ile	Ser
			100					105					110		
Glu	Lys	Thr	Ser	Asp	Gln	Ile	His	Phe	Phe	Phe	Ala	Lys	Leu	Asn	Cys
		115				120						125			
Arg	Leu	Tyr	Arg	Lys	Ala	Asn	Lys	Ser	Ser	Lys	Leu	Val	Ser	Ala	Asn
						135					140				
Arg	Leu	Phe	Gly	Asp	Lys	Ser	Leu	Thr	Phe	Asn	Glu	Thr	Tyr	Gln	Asp
145					150					155				160	
Ile	Ser	Glu	Leu	Val	Tyr	Gly	Ala	Lys	Leu	Gln	Pro	Leu	Asp	Phe	Lys
				165					170					175	
Glu	Asn	Ala	Glu	Gln	Ser	Arg	Ala	Ala	Ile	Asn	Lys	Trp	Val	Ser	Asn
			180					185					190		
Lys	Thr	Glu	Gly	Arg	Ile	Thr	Asp	Val	Ile	Pro	Ser	Glu	Ala	Ile	Asn
		195					200					205			
Glu	Leu	Thr	Val	Leu	Val	Leu	Val	Asn	Thr	Ile	Tyr	Phe	Lys	Gly	Leu
	210					215					220				
Trp	Lys	Ser	Lys	Phe	Ser	Pro	Glu	Asn	Thr	Arg	Lys	Glu	Leu	Phe	Tyr
225					230					235				240	
Lys	Ala	Asp	Gly	Glu	Ser	Cys	Ser	Ala	Ser	Met	Met	Tyr	Gln	Glu	Gly
				245					250					255	
Lys	Phe	Arg	Tyr	Arg	Arg	Val	Ala	Glu	Gly	Thr	Gln	Val	Leu	Glu	Leu
			260					265					270		
Pro	Phe	Lys	Gly	Asp	Asp	Ile	Thr	Met	Val	Leu	Ile	Leu	Pro	Lys	Pro
		275					280					285			
Glu	Lys	Ser	Leu	Ala	Lys	Val	Glu	Lys	Glu	Leu	Thr	Pro	Glu	Val	Leu
	290					295					300				
Gln	Glu	Trp	Leu	Asp	Glu	Leu	Glu	Glu	Met	Met	Leu	Val	Val	His	Met
305					310					315				320	
Pro	Arg	Phe	Arg	Ile	Glu	Asp	Gly	Phe	Ser	Leu	Lys	Glu	Gln	Leu	Gln
				325					330					335	
Asp	Met	Gly	Leu	Val	Asp	Leu	Phe	Ser	Pro	Glu	Lys	Ser	Lys	Leu	Pro
			340					345					350		
Gly	Ile	Val	Ala	Glu	Gly	Arg	Asp	Leu	Tyr	Val	Ser	Asp	Ala	Phe	
		355					360				365				
His	Lys	Ala	Phe	Leu	Glu	Val	Asn	Glu	Glu	Gly	Ser	Glu	Ala	Ala	Ala
	370					375					380				
Ser	Thr	Ala	Leu	Glu	Ala	Tyr	Gly	Arg	Ser	Leu	Asn	Pro	Asn	Arg	Val
385					390					395				400	
Thr	Phe	Lys	Ala	Asn	Arg	Pro	Phe	Leu	Val	Phe	Ile	Arg	Glu	Val	Pro
				405					410					415	

Leu Asn Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys  
420 425 430

<210> 88  
<211> 423  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 88

Arg	Asp	Ile	Pro	Val	Asn	Pro	Ile	Cys	Ile	Tyr	Arg	Asn	Pro	Glu	Lys
1				5				10						15	
Lys	Pro	Gln	Glu	Arg	Arg	Gly	Ala	Gly	Ala	Gly	Glu	Gly	Gln	Asp	Pro
		20						25					30		
Gly	Val	His	Lys	Pro	Pro	Val	Trp	Glu	Leu	Ser	Arg	Ala	Asn	Ser	Arg
		35					40					45			
Phe	Ala	Val	Val	Phe	Tyr	Lys	His	Leu	Ala	Asp	Ser	Lys	Asp	Asn	Glu
	50					55					60				
Glu	Asn	Ile	Phe	Leu	Ser	Pro	Leu	Ser	Ile	Ser	Thr	Ala	Phe	Ala	Met
65					70					75					80
Thr	Lys	Leu	Gly	Ala	Cys	Gly	Asp	Thr	Leu	Gln	Gln	Leu	Met	Glu	Val
				85					90					95	
Phe	Gln	Phe	Asp	Thr	Ile	Ser	Glu	Lys	Thr	Ser	Asp	Gln	Val	His	Phe
			100					105					110		
Phe	Phe	Ala	Lys	Leu	Asn	Cys	Arg	Leu	Tyr	Lys	Lys	Ala	Asn	Lys	Ser
		115					120					125			
Ser	Glu	Leu	Ile	Ser	Ala	Asn	Arg	Leu	Phe	Gly	Glu	Lys	Ser	Leu	Val
	130					135					140				
Phe	Asn	Glu	Thr	Tyr	Gln	Asn	Ile	Ser	Glu	Ile	Val	Tyr	Gly	Ala	Lys
145					150					155					160
Leu	Trp	Pro	Leu	Asn	Phe	Lys	Glu	Lys	Pro	Glu	Leu	Ser	Arg	Lys	Ile
				165					170					175	
Ile	Asn	Glu	Trp	Val	Ala	Asn	Lys	Thr	Glu	Arg	Arg	Ile	Thr	Glu	Val
			180					185					190		
Ile	Pro	Glu	Lys	Gly	Ile	Asp	Asp	Leu	Thr	Val	Leu	Val	Leu	Val	Asn
		195					200					205			
Thr	Ile	Tyr	Phe	Lys	Gly	His	Trp	Lys	Ser	Gln	Phe	Pro	Ala	Pro	Asn
	210					215					220				
Thr	Arg	Leu	Asp	Leu	Phe	His	Lys	Ala	Asn	Gly	Glu	Thr	Cys	Asn	Val
225					230					235					240
Pro	Ile	Met	Tyr	Gln	Glu	Ser	Arg	Phe	Pro	Tyr	Ala	Phe	Ile	Gln	Glu
				245					250					255	
Asp	Lys	Val	Gln	Val	Leu	Glu	Leu	Pro	Tyr	Lys	Gly	Asp	Asp	Ile	Thr
			260					265					270		
Met	Val	Leu	Val	Leu	Pro	Lys	Ala	Gly	Thr	Pro	Leu	Val	Glu	Val	Glu
							280					285			
Arg	Asp	Leu	Thr	Ser	Asp	Lys	Leu	Gln	Asp	Trp	Ile	Asp	Ser	Met	Met
	290					295					300				
Glu	Val	Ser	Leu	Thr	Val	Ser	Phe	Pro	Arg	Phe	Arg	Val	Glu	Asp	Ser
305					310					315					320
Phe	Ser	Val	Lys	Glu	Lys	Leu	Arg	Lys	Met	Gly	Leu	Glu	Asp	Leu	Phe
				325					330					335	
Ser	Pro	Glu	Asn	Ala	Lys	Leu	Pro	Gly	Ile	Val	Ala	Gly	Asp	Arg	Thr
			340					345					350		
Asp	Leu	Tyr	Val	Ser	Glu	Ala	Phe	His	Lys	Ala	Phe	Leu	Glu	Val	Asn
		355					360					365			
Glu	Glu	Gly	Ser	Glu	Ala	Ser	Ala	Ala	Thr	Ala	Val	Val	Ile	Ser	Gly
	370					375					380				
Arg	Ser	Phe	Pro	Met	Asn	Arg	Ile	Ile	Phe	Glu	Ala	Asn	Arg	Pro	Phe

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385                      390                      395                      400  
 Leu Leu Phe Ile Arg Glu Ala Thr Leu Asn Thr Ile Ile Phe Met Gly  
                          405                      410                      415  
 Arg Ile Ser Asp Pro Cys Ser

<210> 89  
 <211> 456

<212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/note =  
                  synthetic construct

<400> 89  
 Met Tyr Leu Leu Ser Leu Leu Leu Leu Ser Leu Leu Gly Ser Ala Tyr  
   1                          5                          10                          15  
 Leu Gln Pro Gln His Ala Asp Ile Cys Leu Ala Lys Pro Lys Asp Ile  
                           20                          25                          30  
 Pro Leu Thr Pro Met Cys Val Tyr Arg Lys Pro Leu Glu Val Val Glu  
                           35                          40                          45  
 Thr Glu Glu Lys Glu Lys Glu Pro Thr Thr Gln Glu Gln Lys Val Pro  
                           50                          55                          60  
 Glu Ser Thr Asn Pro Arg Val Tyr Glu Leu Ser Gln Ala Asn Ala Lys  
   65                          70                          75                          80  
 Phe Ala Ile Ala Phe Tyr Lys Asn Leu Ala Asp Ser Lys Arg Asp Lys  
                           85                          90                          95  
 Glu Asn Ile Phe Met Ser Pro Leu Ser Ile Ser Gln Ala Phe Thr Met  
                           100                          105                          110  
 Ala Lys Leu Gly Ala Cys Asn Asn Thr Leu Lys Gln Leu Met Glu Val  
                           115                          120                          125  
 Phe His Phe Asp Thr Val Ser Glu Arg Ala Ser Asp Gln Ile His Tyr  
                           130                          135                          140  
 Phe Phe Ala Lys Leu Asn Cys Arg Leu Phe Arg Lys Ala Asn Lys Ser  
   145                          150                          155                          160  
 Ser Glu Leu Val Ser Val Asn Arg Leu Phe Gly Glu Lys Ser Leu Thr  
                           165                          170                          175  
 Phe Asn Glu Thr Tyr Gln Asp Ile Ser Glu Ile Val Tyr Gly Ala Lys  
                           180                          185                          190  
 Leu Trp Pro Leu Asn Phe Arg Asp Lys Pro Glu Leu Ser Arg Glu Ile  
                           195                          200                          205  
 Ile Asn Asn Trp Val Ser Asn Lys Thr Glu Lys Arg Ile Thr Asp Val  
                           210                          215                          220  
 Ile Pro Lys Asp Ala Ile Thr Pro Asp Thr Val Leu Val Leu Ile Asn  
   225                          230                          235                          240  
 Ala Ile Tyr Phe Lys Gly Leu Trp Lys Ser Lys Phe Asn Ser Glu Asn  
                           245                          250                          255  
 Thr Lys Met Asp Gln Phe His Pro Ala Lys Asn Ser Asn Cys Leu Thr  
                           260                          265                          270  
 Ala Thr Met Tyr Gln Glu Gly Thr Phe Arg Tyr Gly Ser Phe Lys Asp  
                           275                          280                          285  
 Asp Gly Val Gln Val Leu Glu Leu Pro Tyr Lys Gly Asp Asp Ile Thr  
                           290                          295                          300  
 Met Val Leu Val Leu Pro Ser Gln Glu Thr Pro Leu Thr Thr Val Glu  
   305                          310                          315                          320  
 Gln Asn Leu Thr Leu Glu Lys Leu Gly Asn Trp Leu Gln Lys Ser Arg  
                           325                          330                          335  
 Glu Leu Gln Leu Ser Val Tyr Leu Pro Arg Phe Arg Val Glu Asp Ser  
                           340                          345                          350  
 Phe Ser Val Lys Glu Lys Leu Gln Glu Met Gly Leu Val Asp Leu Phe  
                           355                          360                          365

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Asp Pro Asn Ser Ala Lys Leu Pro Gly Ile Ile Ala Gly Gly Arg Thr  
 370 375 380  
 Asp Leu Tyr Val Ser Asp Ala Phe His Lys Ala Phe Leu Glu Val Asn  
 385 390 395 400  
 Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr Ala Val Ile Leu Thr Gly  
 405 410 415  
 Arg Ser Leu Asn Leu Asn Arg Ile Ile Phe Arg Ala Asn Arg Pro Phe  
 420 425 430  
 Leu Val Phe Ile Arg Glu Val Ala Ile Asn Ala Ile Leu Phe Met Gly  
 435 440 445  
 Arg Val Ala Asn Pro Cys Thr Glu  
 450 455

<210> 90

<211> 465

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
 synthetic construct

<400> 90

Met Tyr Ser Pro Gly Ala Gly Ser Gly Ala Ala Gly Glu Arg Lys Leu  
 1 5 10 15  
 Cys Leu Leu Ser Leu Leu Leu Ile Gly Ala Leu Gly Cys Ala Ile Cys  
 20 25 30  
 His Gly Asn Pro Val Asp Asp Ile Cys Ile Ala Lys Pro Arg Asp Ile  
 35 40 45  
 Pro Val Asn Pro Leu Cys Ile Tyr Arg Ser Pro Gly Lys Lys Ala Thr  
 50 55 60  
 Glu Glu Asp Gly Ser Glu Gln Lys Val Pro Glu Ala Thr Asn Arg Arg  
 65 70 75 80  
 Val Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Asn Phe Tyr  
 85 90 95  
 Gln His Leu Ala Asp Ser Lys Asn Asp Asn Asn Ile Phe Leu Ser  
 100 105 110  
 Pro Leu Ser Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys  
 115 120 125  
 Asn Asp Thr Leu Lys Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile  
 130 135 140  
 Ser Glu Lys Thr Ser Asp Gln Ile His Phe Phe Ala Lys Leu Asn  
 145 150 155 160  
 Cys Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser Asp Leu Val Ser Ala  
 165 170 175  
 Asn Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Ser Tyr Gln  
 180 185 190  
 Asp Val Ser Glu Val Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe  
 195 200 205  
 Lys Glu Asn Pro Glu Gln Ser Arg Val Thr Ile Asn Asn Trp Val Ala  
 210 215 220  
 Asn Lys Thr Glu Gly Arg Ile Lys Asp Val Ile Pro Gln Gly Ala Ile  
 225 230 235 240  
 Asn Glu Leu Thr Ala Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly  
 245 250 255  
 Leu Trp Lys Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Pro Phe  
 260 265 270  
 Tyr Lys Val Asp Gly Gln Ser Cys Pro Val Pro Met Met Tyr Gln Glu  
 275 280 285  
 Gly Lys Phe Lys Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu  
 290 295 300  
 Leu Pro Phe Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys

Pro	Glu	Lys	Ser	Leu 325	Ala	Lys	Val	Glu	Gln	Glu	Leu	Thr	Pro	Glu
Leu	Gln	Glu	Trp 340	Leu	Asp	Glu	Leu	Ser 345	Glu	Thr	Met	Leu	Val 350	His
Met	Pro	Arg 355	Phe	Arg	Thr	Glu	Asp 360	Gly	Phe	Ser	Leu	Lys 365	Glu	Gln
Gln	Asp 370	Met	Gly	Leu	Ile	Asp 375	Leu	Phe	Ser	Pro	Glu 380	Lys	Ser	Gln
Pro 385	Gly	Ile	Val	Ala	Gly 390	Gly	Arg	Asp	Asp	Leu 395	Tyr	Val	Ser	Asp
Phe	His	Lys	Ala	Phe 405	Leu	Glu	Val	Asn	Glu 410	Glu	Gly	Ser	Glu	Ala
Ala	Ser	Thr	Ser 420	Val	Val	Ile	Thr	Gly 425	Arg	Ser	Leu	Asn	Pro 430	Asn
val	Thr	Phe 435	Lys	Ala	Asn	Arg	Pro 440	Phe	Leu	Val	Leu	Ile 445	Arg	Glu
Ala	Leu 450	Asn	Thr	Ile	Ile	Phe 455	Met	Gly	Arg	Val	Ala 460	Asn	Pro	Cys
Asn 465							.							

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<210> 91
<211> 1599
<212> DNA
<213> Artificial sequence
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<220>  
<223> Description of Artificial Sequence:/note =  
synthetic construct

<400>	91					
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ggcggattgc	ctcagatcac	actatctcca	cttgcccagc	cctgtggaag	attagcggcc	120
atgtattcca	atgtgatagg	aactgtaacc	tctggaataa	ggaagcgtta	tcttttgtcc	180
ttgctgctca	tgggctcttg	ggactgctg	acctgtcacg	ggagccctgt	ggacatctgc	240
acagccaagc	cgcgggacat	tcccatggaat	cccatgtgca	tttaccgctc	cccggagaag	300
aaggcaactg	aggatgaggg	ctcagaacag	aagatcccgg	aggccacca	ccggcggtgc	360
tgggaactgt	ccaaggccaa	ttcccgcgtt	gctaccactt	tctatccaga	cctggcagat	420
tccaagaagt	acaattgata	catttttctg	tcacccttga	gtatctccac	ggcttttgtc	480
atgaccaagc	tgggtgcctg	taatgacacc	ctccagcaac	tgatggaggt	atttaagttt	540
gacaccatat	ctgagaaaac	atctgatcag	atccactttc	tctttgccaa	actgaactgc	600
cgactctatc	gaaaagccaa	caaatctctc	aagttagtat	cagccaatcg	cctttttgga	660
gacaaatccc	ttaccttcaa	tgagacctac	caggacatca	gtgagttggt	atatggagcc	720
aagctccagc	ccctggactt	caaggaaaat	gcagagcaat	ccagagcggc	catcaacaaa	780
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ttcagccctg	agaacacaa	gaaggaaactg	ttctacaagg	ctgatggaga	gtcgtgttca	960
gcatctatga	tgtaccagga	aggcaagttc	cgttatcgcc	gcgtggctga	aggccaccga	1020
gtgcttgagt	tgcccttcaa	aggtgatgac	atcaccatgg	tctctatctt	gcccgaagcct	1080
gagaagagcc	tggccaaggt	ggagaaggaa	ctcaccctag	aggtgctgca	ggagtggctg	1140
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ttcagtttga	aggagcagct	gcaagacatg	ggccttgtcg	atctgtttcag	ccctgaaaag	1260
tccaactctc	caggttagtt	tgcagaaggg	cgagatgacc	tctatgtctc	agatgcattc	1320
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gtgattgctg	gccgttcgct	aaaccccaac	agggtgactt	tcaaggccaa	caggcccttc	1440
ctggttttta	taagagaagt	tcctctgaac	actattatct	tcattggcag	agtagccaac	1500
ccttgtgtta	ataaaaaagt	tcttattctt	tgcactctct	cctatttttg	gtttgtgaac	1560
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<210>	92
<211>	430
<212>	PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;221&gt; VARIANT

&lt;222&gt; (386)...(389)

&lt;223&gt; Xaa = any amino acid

&lt;400&gt; 92

Ser	Pro	Val	Asp	Ile	Cys	Thr	Ala	Lys	Pro	Arg	Asp	Ile	Pro	Met	Asn
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Pro	Met	Cys	Ile	Tyr	Arg	Ser	Pro	Glu	Lys	Lys	Ala	Thr	Glu	Asp	Glu
			20					25					30		
Gly	Ser	Glu	Gln	Lys	Ile	Pro	Glu	Ala	Thr	Asn	Arg	Arg	Val	Trp	Glu
		35					40					45			
Leu	Ser	Lys	Ala	Asn	Ser	Arg	Phe	Ala	Thr	Thr	Phe	Tyr	Gln	His	Leu
	50					55					60				
Ala	Asp	Ser	Lys	Asn	Asp	Asn	Asp	Asn	Ile	Phe	Leu	Ser	Pro	Leu	Ser
65					70					75					80
Ile	Ser	Thr	Ala	Phe	Ala	Met	Thr	Lys	Leu	Gly	Ala	Cys	Asn	Asp	Thr
			85						90					95	
Leu	Gln	Gln	Leu	Met	Glu	Val	Phe	Lys	Phe	Asp	Thr	Ile	Ser	Glu	Lys
			100					105					110		
Thr	Ser	Asp	Gln	Ile	His	Phe	Phe	Phe	Ala	Lys	Leu	Asn	Cys	Arg	Leu
		115					120					125			
Tyr	Arg	Lys	Ala	Asn	Lys	Ala	Ser	Lys	Leu	Val	Ser	Ala	Asn	Arg	Leu
	130					135					140				
Phe	Gly	Asp	Lys	Ser	Leu	Thr	Phe	Asn	Glu	Thr	Tyr	Gln	Asp	Ile	Ser
145					150					155					160
Glu	Leu	Val	Tyr	Gly	Ala	Lys	Leu	Gln	Pro	Leu	Asp	Phe	Lys	Glu	Asn
				165					170					175	
Ala	Glu	Gln	Ser	Arg	Ala	Ala	Ile	Asn	Lys	Trp	Val	Ser	Asn	Lys	Thr
			180					185					190		
Glu	Gly	Arg	Ile	Thr	Asp	Val	Ile	Pro	Ser	Glu	Ala	Ile	Asn	Glu	Leu
		195					200					205			
Thr	Val	Leu	Val	Leu	Val	Asn	Thr	Ile	Tyr	Phe	Lys	Gly	Leu	Trp	Lys
	210					215					220				
Ser	Lys	Phe	Ser	Pro	Glu	Asn	Thr	Arg	Lys	Glu	Leu	Phe	Tyr	Lys	Ala
225					230					235					240
Asp	Gly	Glu	Ser	Cys	Ser	Ala	Ser	Met	Met	Tyr	Gln	Glu	Gly	Lys	Phe
				245					250					255	
Arg	Tyr	Arg	Arg	Val	Ala	Glu	Gly	Thr	Gln	Val	Leu	Glu	Leu	Pro	Phe
			260					265					270		
Lys	Gly	Asp	Asp	Ile	Thr	Met	Val	Leu	Ile	Leu	Pro	Lys	Pro	Glu	Lys
		275					280					285			
Ser	Leu	Ala	Lys	Val	Glu	Lys	Glu	Leu	Thr	Pro	Glu	Val	Leu	Gln	Glu
	290					295					300				
Trp	Leu	Asp	Glu	Leu	Glu	Glu	Met	Met	Leu	Val	Val	His	Met	Pro	Arg
305					310					315					320
Phe	Arg	Ile	Glu	Asp	Gly	Phe	Ser	Leu	Lys	Glu	Gln	Leu	Gln	Asp	Met
				325					330					335	
Gly	Leu	Val	Asp	Leu	Phe	Ser	Pro	Glu	Lys	Ser	Lys	Leu	Pro	Gly	Ile
			340					345					350		
Val	Ala	Glu	Gly	Arg	Asp	Asp	Leu	Tyr	Val	Ser	Asp	Ala	Phe	His	Lys
		355					360					365			
Ala	Phe	Leu	Glu	Val	Asn	Glu	Glu	Gly	Ser	Glu	Ala	Ala	Ala	Ser	Thr
	370					375					380				
Ala	Xaa	Xaa	Xaa	Xaa	Gly	Arg	Ser	Leu	Asn	Pro	Asn	Arg	Val	Thr	Phe
385					390					395					400
Lys	Ala	Asn	Arg	Pro	Phe	Leu	Val	Phe	Ile	Arg	Glu	Val	Pro	Leu	Asn
				405					410					415	

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Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys  
 420 425 430

<210> 93

<211> 430

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
 synthetic construct

<400> 93

Ser	Pro	Val	Asp	Ile	Cys	Thr	Ala	Lys	Pro	Arg	Asp	Ile	Pro	Met	Asn
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Pro	Met	Cys	Ile	Tyr	Arg	Ser	Pro	Glu	Lys	Lys	Ala	Thr	Glu	Asp	Glu
			20					25					30		
Gly	Ser	Glu	Gln	Lys	Ile	Pro	Glu	Ala	Thr	Asn	Arg	Arg	Val	Trp	Glu
		35					40					45			
Leu	Ser	Lys	Ala	Asn	Ser	Arg	Phe	Ala	Thr	Thr	Phe	Tyr	Gln	His	Leu
	50					55					60				
Ala	Asp	Ser	Lys	Asn	Asp	Asn	Asp	Asn	Ile	Phe	Leu	Ser	Pro	Leu	Ser
65				70						75					80
Ile	Ser	Thr	Ala	Phe	Ala	Met	Thr	Lys	Leu	Gly	Ala	Cys	Asn	Asp	Thr
				85					90					95	
Leu	Gln	Gln	Leu	Met	Glu	Val	Phe	Lys	Phe	Asp	Thr	Ile	Ser	Glu	Lys
			100					105					110		
Thr	Ser	Asp	Gln	Ile	His	Phe	Phe	Phe	Ala	Lys	Leu	Asn	Cys	Arg	Leu
		115					120					125			
Tyr	Arg	Lys	Ala	Asn	Lys	Ala	Ser	Lys	Leu	Val	Ser	Ala	Asn	Arg	Leu
		130				135					140				
Phe	Gly	Asp	Lys	Ser	Leu	Thr	Phe	Asn	Glu	Thr	Tyr	Gln	Asp	Ile	Ser
145					150					155					160
Glu	Leu	Val	Tyr	Gly	Ala	Lys	Leu	Gln	Pro	Leu	Asp	Phe	Lys	Glu	Asn
				165					170					175	
Ala	Glu	Gln	Ser	Arg	Ala	Ala	Ile	Asn	Lys	Trp	Val	Ser	Asn	Lys	Thr
			180					185					190		
Glu	Gly	Arg	Ile	Thr	Asp	Val	Ile	Pro	Ser	Glu	Ala	Ile	Asn	Glu	Leu
		195					200					205			
Thr	Val	Leu	Val	Leu	Val	Asn	Thr	Ile	Tyr	Phe	Lys	Gly	Leu	Trp	Lys
	210					215					220				
Ser	Lys	Phe	Ser	Pro	Glu	Asn	Thr	Arg	Lys	Glu	Leu	Phe	Tyr	Lys	Ala
225					230					235					240
Asp	Gly	Glu	Ser	Cys	Ser	Ala	Ser	Met	Met	Tyr	Gln	Glu	Gly	Lys	Phe
				245					250					255	
Arg	Tyr	Arg	Arg	Val	Ala	Glu	Gly	Thr	Gln	Val	Leu	Glu	Leu	Pro	Phe
			260					265					270		
Lys	Gly	Asp	Asp	Ile	Thr	Met	Val	Leu	Ile	Leu	Pro	Lys	Pro	Glu	Lys
		275					280					285			
Ser	Leu	Ala	Lys	Val	Glu	Lys	Glu	Leu	Thr	Pro	Glu	Val	Leu	Gln	Glu
	290					295					300				
Trp	Leu	Asp	Glu	Leu	Glu	Glu	Met	Met	Leu	Val	Val	His	Met	Pro	Arg
305					310					315					320
Phe	Arg	Ile	Glu	Asp	Gly	Phe	Ser	Leu	Lys	Glu	Gln	Leu	Gln	Asp	Met
				325					330					335	
Gly	Leu	Val	Asp	Leu	Phe	Ser	Pro	Glu	Lys	Ser	Lys	Leu	Pro	Gly	Ile
			340					345					350		
Val	Ala	Glu	Gly	Arg	Asp	Asp	Leu	Tyr	Val	Ser	Asp	Ala	Phe	His	Lys
		355					360					365			
Ala	Phe	Leu	Glu	Val	Asn	Glu	Gly	Ser	Glu	Ala	Ala	Ala	Ser	Thr	
	370					375				380					
Ala	Val	Val	Ile	Ala	Gly	Arg	Ser	Leu	Asn	Pro	Asn	Arg	Val	Thr	Phe

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385					390					395					400
Lys	Ala	Asn	Arg	Pro	Phe	Leu	Val	Phe	Ile	Arg	Glu	Val	Pro	Leu	Asn
				405					410					415	
Thr	Ile	Ile	Phe	Met	Gly	Arg	Val	Ala	Asn	Pro	Cys	Val	Lys		
			420					425					430		